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OM nucleic - nucleic search, using sw model

Run on: September 1, 2000, 01:15:48 ; Search time 261.02 Seconds

(without alignments)  
4326.089 Million cell updates/sec

Title: US-09-171-553-3

Perfect score: 8209

Sequence: 1 gtagtgcacgactgtggcc.....aaaaaaaaaaaaaaaaaaaa 8209

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 243080 segs, 68777915 residues

Total number of hits satisfying chosen parameters: 486160

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: /cgn2\_6/ptodata/2/lna/5A.COMB.seq:\*  
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7: /cgn2\_6/ptodata/2/lna/Backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Rank	Score	Query Match	Length	ID	Description
1	2244.4	27.3	8535	US-08-716-351A-1	Sequence 1, Appl1
2	1747	21.3	8333	US-08-110-300A-8	Sequence 8, Appl1
3	1747	21.3	8333	US-08-886-642-8	Sequence 8, Appl1
4	1747	21.3	8333	PCT-US93-08041-8	Sequence 8, Appl1
5	1738.8	21.2	8202	US-08-258-420-13	Sequence 13, Appl1
6	1687.4	20.6	8332	US-08-850-961-1	Sequence 1, Appl1
7	1596	19.4	10367	US-08-110-300A-9	Sequence 9, Appl1
8	1596	19.4	10367	US-08-886-642-9	Sequence 9, Appl1
9	1596	19.4	10367	PCT-US93-08041-9	Sequence 9, Appl1
10	852.6	10.4	3674	US-08-105-483-324	Sequence 324, App
11	852.6	10.4	3674	US-08-709-209-324	Sequence 324, App
12	852.6	10.4	3674	US-08-458-101-324	Sequence 324, App
13	815.4	9.9	6363	US-08-929-967-6	Sequence 6, Appl1
14	359.4	4.4	10970	US-08-716-351A-5	Sequence 5, Appl1
15	303.8	3.7	1965	US-08-258-420-9	Sequence 9, Appl1
16	301.4	3.7	2499	US-08-105-483-310	Sequence 310, App
17	301.4	3.7	2499	US-08-709-209-310	Sequence 310, App
18	301.4	3.7	2499	US-08-458-101-310	Sequence 310, App
19	300.6	3.7	2001	US-08-850-961-13	Sequence 13, Appl1
20	298.8	3.6	949	PCT-US91-08254-1	Sequence 1, Appl1
21	298.8	3.6	949	PCT-US91-08254-2	Sequence 2, Appl1
22	298.2	3.6	1911	US-08-258-420-8	Sequence 8, Appl1
23	290.2	3.5	1914	US-08-258-420-7	Sequence 7, Appl1
24	274.8	3.3	789	US-08-181-335B-3	Sequence 3, Appl1
25	274.8	3.3	789	US-08-181-335B-5	Sequence 5, Appl1
26	274.8	3.3	789	US-08-181-335B-6	Sequence 6, Appl1

27	274.8	3.3	789	6	PCT-US95-00129-3	Sequence 3, Appl1
28	274.8	3.3	789	6	PCT-US95-00129-5	Sequence 5, Appl1
29	274.8	3.3	789	6	PCT-US95-00129-6	Sequence 6, Appl1
30	233	2.8	735	2	US-08-798-000-3	Sequence 3, Appl1
31	226.6	2.8	1234	2	US-08-798-000-1	Sequence 1, Appl1
32	222.2	2.7	1237	2	US-08-798-000-2	Sequence 2, Appl1
33	192	2.3	5109	1	US-08-073-836-1	Sequence 1, Appl1
34	192	2.3	5176	1	US-08-073-836-2	Sequence 2, Appl1
35	176.4	2.1	2391	5	US-08-691-563C-57	Sequence 57, Appl1
36	165.6	2.0	2448	5	US-08-691-563C-53	Sequence 53, Appl1
37	162.6	2.0	8387	3	US-08-532-814-1	Sequence 1, Appl1
38	157.2	1.9	10306	5	US-08-716-351A-4	Sequence 4, Appl1
39	149.6	1.8	1167	5	US-08-691-563C-61	Sequence 61, Appl1
40	149.6	1.8	1158	2	US-08-471-724-1	Sequence 1, Appl1
41	149.6	1.8	1158	3	US-08-471-968-1	Sequence 1, Appl1
42	149.6	1.8	1158	4	US-08-384-137-1	Sequence 1, Appl1
43	149.6	1.8	1158	4	US-08-470-006A-1	Sequence 1, Appl1
44	149.6	1.8	1158	5	US-08-691-563C-1	Sequence 1, Appl1
45	144.4	1.8	9661	5	US-08-716-351A-3	Sequence 3, Appl1

## ALIGNMENTS

RESULT 1  
US-08-716-351A-1  
Sequence 1, Application US/08716351A  
Patent No. 6033905  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: Gibbon Ape Leukemia Virus-Based  
TITLE OF INVENTION: Retroviral Vectors  
NUMBER OF SEQUENCES: 5  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/716,351A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/03784  
FILING DATE: 06-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Bastien, Kevin L.  
REGISTRATION NUMBER: 34,774  
REFERENCE/DOCKET NUMBER: 15280-128-1PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ. ID NO. 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8535 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: misc.feature  
LOCATION: 1..8535  
OTHER INFORMATION: /standard\_name= "GALV SEATO Genome"

Query Match 27.3%; Score 2244.4; DB 5; Length 8535;  
Best Local Similarity 59.1%; Pred. No. 0;  
Matches 4366; Conservative 0; Mismatches 2811; Indels 215; Gaps 22;

0y 332 agcagagctcgtgaggtacacagcgtcccccggggagccgggggggagga 391  
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Qy	392	gagcagagagagcagcctgg	tgctcctactgctgcgcagagacgagcttg	tgtgttggaa	451
Db	816	GGACCAAGGAGCGCCTGGTGGAC	CTCCG-----GTAAAGGGCGTTGTGACCG	864	
Qy	452	gcgaagcttcccccccgcgccg	ctccgactcttgcgcgttggagagagcgagac	511	
Db	865	ATTTCACTGCCCTCGGTGTAAC	GGCGCTCTGATCTCATTTCTCTCTCTCGTGGCCTCG	924	
Qy	512	gggcgcgtgtgctgagactgt	tggtttctgctcgtgtgttctgtgtgctgt	571	
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Qy	572	tgctacagtttaataatg	ggacagacagtgactaccccccttggttgcctgcgcga	631	
Db	985	CTCCCAATATCATATATGGG	AGACAAATATTCACCCCTATCTCCCTCATCTTAATCA	1044	
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Db	1222	ACATCCGGACCAAGTTCC	ATATATCTGTGATATGGCAGCACTCGCCCAAGATCCCCAC	1281	
Qy	872	atgggttaaacacatg	ctataataaccgaagaagccaggtcccgcaatccgtgtcttg	931	
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Qy	932	agagaaaaaacaacac	ctcgcgcgaaaaagtgcagcccttctcgtatctacaccgcga	991	
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Db	1882	CATTAAATGAGGCCCTTCCCTCATATGACCTACTGCGGTTTACAACACAGCCGACAGTAG	1941
QY	1526	ggaagactggaatatcatatcgccagagctctggctggcggctctccggggcgccctaaagc	1585
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QY	1586	gcccactaatcttgctctaaagtgaaagagatgtatgcagggagcccgaaacgaaactccctcgt	1645
Db	2002	TCTTACCAATTTGGCTTAAGGTAAAGAGAGGCTTTGCAAGGAGCCGACGAACCCCTTGCT	2061
QY	1646	attctctgagagggctcttgaaagcccttcagcggtctcaccctcttgatctctacccaga	1705
Db	2062	TTTCTTTGAACCCCTGTATGACAGGCTTATAGAGATATACATCTCGTTTGAATTCCTTTGCA	2121
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Db 6224 AACCGATGCTGCTCT--CTAAGCAGTCACAGCTCCGGACTGACAGCTATCTGCGGT 6281  
Qy 5950 ttcctatgtcccaagcagagaaagaaatactgtggtgtgttctgtggaaatccctc 6009  
Db 6282 TATTAACCAATCACTGGGAGACATAGGTTGACGCTACCTCGGCTAGCAATG 6341  
Qy 6010 tctagaagatgagctgcgtgtcactccacagtgt----- 6044  
Db 6342 GCAAGCTTACCTTCTACGATGTCTCCCGGATGGCGGACCTTTCAGAACTGAAAG 6401  
Qy 6045 -----agactggaatgtgcgtactctctccagacgg 6079  
Db 6402 TCGGGGGGCTTGAATTCCTATCTGTAAGAATGGGATTTGTAGACCGGAGCCGT 6461  
Qy 6080 taaatctccttctgtcaattccgcgcgggcaagtaacaaatgtataatgaag 6139  
Db 6462 TATTGGCTATCTAAATCTCAAAAGACCTCATTAATAATGGGACCAATAAGCGAA 6521  
Qy 6140 atagagctgtcccaatcagactagattatcctaaagtaagttcactgaaagaa 6199  
Db 6522 TGGACTCAAAAATTTTAAACAGTGTACCAAGCGCTGTGTATACCCCTTAAATAGT 6581  
Qy 6200 caggaataatactcaaaagtgtataaagtgtatgtcgtgggaata-----gttttata 6255  
Db 6582 TTCACAGACAAAGAAATTAATCCAAAGAGACTGATTAACGGAAACATCGGGGATTAAG 6641  
Qy 6256 tatgtcgggagcaggtgtccacttaaccatcgccttagatagtagagcgggagaa 6315  
Db 6642 TTCTATGTGTCTGAGATTCAGGCGTACAGTTCCATTCACATTCGCTTAAATAATCAACAACATG 6701  
Qy 6316 cccctgtgtcaatgtgacccgttaagtaagtgtcgtgcaaggt-----gcc 6363  
Db 6702 CCAAGCTGTGACATGAGTCTGTGACCTGTGCTTGTGAAACAGAGACCTCTAGAACGTGC 6761  
Qy 6364 ccgacctgtgagcagcagcgaataactgtgcgtgtcccaatlaacctcgtgtgcgtgac 6423  
Db 6762 CTGCTCTCCACACTCTCTCTCCCAAGGAGGCGCAACCGCATCTCTCCCGACT 6821  
Qy 6424 ataacagcgcgtcagcaagtaacactgtatgtatcctcaacaacgcctagaac 6483  
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Qy 6484 tcccaaggttctcgtttaaagacagagagactcttcaagctcatcagagagcttc 6543  
Db 6882 CTAAACACTCCGCTCCACACAGGAGACACTTTTGTATTTGTGAGGGGCGCTTC 6941  
Qy 6544 caagccaactcaactcagcagctgtatgcacttcttctgtgtgttctgtatcctca 6603  
Db 6942 CTAACTTAAATGTATGCAACCAAGGGCCACTGAGTGTGCTGTGTGTTGGCCATG 7001  
Qy 6604 gggctccttattatagggagatgtgttaaagaaagaaatcaatgtgacaaagagat 6663  
Db 7002 GGCCCCCTTATTAATGAAGAAATAGCTTCATGAGGAGGTCCCTACATCCACGACCTT 7061  
Qy 6664 agaatatgatactgtgggttcggaaataagcttcaactcaactgaagtttccggaag 6723  
Db 7062 ---GACGGTGGCGCTGGGGACCAAGAAAGCTCACTCACTCAAGTGTGAGACAC 7118  
Qy 6724 ggtacatgtcataggaagctccccaatcccaacaacacttgcatagtatgtgtgt 6783  
Db 7119 GCGTTGTGATAGAAAGTCCCTTTACCATACAGATCTGCAATGAGACCTATCC 7178  
Qy 6784 tatgagcagcctcagaaatagttatgtactcgtgtataacaggtgtgtgtgtgtc 6843  
Db 7179 ATCAATTCCTCGGAGACATGATGTCTCCCTCCCAACATAGCTGTGTGGCTTGC 7238

Sequence 8, Application US/08110300A  
Patent No. 5643756  
GENERAL INFORMATION:  
APPLICANT: Pinter, Abraham  
APPLICANT: Kayman, Samuel  
TITLE OF INVENTION: FUSION GLYCOPROTEINS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Davis Hoxie Faithfull and Hapgood  
STREET: 45 Rocketteller Pl.  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10111

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/110,300A  
FILING DATE: 20-AUG-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Jacobs, Seth H.  
REGISTRATION NUMBER: 32,140  
REFERENCE/DOCKET NUMBER: 11698A50  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-757-2200  
TELEFAX: 212-586-1461  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8323 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO

Query Match	21.3%	Score 1747:	DB 1:	Length 8323:
Best Local Similarity	55.6%	Pred No. 0:		
Matches 4058:	Conservative	0:	Mismatches 3005:	Indels 238:
				Gaps 27
QY	467	tcgcgagcgctccgactctcttgcgcgtcgttggaga--gacgcgaaaggtgcgcgtgtc	524	
Db	498	TCGCCCCCGCTCGAATTTTTCCTTCGGTTTGGACGAGACGCCGCCCGCGCTTGC	511	
QY	525	ctggacatctgtgttcctcgtcgcggtgtcttctcgtgtgcgcctctgtcctacgtttt	557	
Db	558	CTGCTCAGACATCGTTCTGTGTGTCTGTCTGTTTACAGTGT--TTCTGATTTGTCTGAA	615	
QY	585	aatatgggaacagaacagtgactaccccccttaattgttcctctgcacatttggactgaagt	644	
Db	616	AACATGGGCGAGCGTGTTACACCCCGCTTAAGTTTACCTTTAAGCACCAGGAAGATGTC	675	
QY	645	agatccagggctcaatattgtcagttcaagttcaagaagagacattggagaagcttcgt	704	
Db	676	GAGCGACAGCGCCCAACACTGTGCGTAGAGGTTAGAAAAAGCGCGTTCATTTACATTTCG	735	
QY	705	gcctctgaatggccaacattcgaatgtttgtaigccatcagaaggagaccttaattctgaa	764	
Db	736	TCTCGAAGATGGCCAACTTCACAGTCGGATGACCACAGAGGCGCATTTTAACCCAGAC	795	
QY	765	attatcctgctgtttaagccaatcatttltcagacttgaccgcgctctcactctgatacag	824	
Db	796	ATTATTATACACAGGTTAAGATCAAGGTCCTTCACCTGGCCACATGACATCCGGATCAG	855	
QY	825	gaagccataatccttaacgttgcaaaatttgcgcgaagaatcctccgcacatgtgtctaacaa	884	
Db	856	GTCCTTCATCATGTACTCGGAAAGCTATACCACTAACCCCGCTCCCTGGTCAACACC	915	
QY	885	tggtctaaa-----taaccagaagaagcgaagtcctcccgaaatcctgtgc	925	
Db	916	TTCTGTCAACCTTAACCTCCCTCTCTCTTCCCTTCACCCCTCTCTCCACCTGA	975	
QY	926	tccttgagagaaaaaacaacatcctgcgcgaaaaaagtcgagccctcttctcgtatctacc	985	
Db	976	CCCCACACTCGACCCCGCCCAAGTCTCTCCCTCTATCCGGCTCATCTTCTTCTTAAAC	1035	
QY	986	ccgagatcagaggaacgcgcgacttggccggaacccaacactgttccccaacccctatc	1045	
Db	1036	ACCAAACTCTAGGCGCTCAAGTCTTCTGTATTACGGAGGACACATCATTTGATCTACTACG	1095	
QY	1046	cagacaaggtgtcgtcgaggggaacctctgcctcctcctgagctcgcgtgtgtgtggaggac	1105	

[illegible]





